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TECH CENTER 1600/2900

P. Jung
 RAW SEQUENCE LISTING DATE: 04/17/2001
 PATENT APPLICATION: US/09/459,573 TIME: 11:24:37

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 Output Set: N:\CRF3\04172001\I459573.raw

ENTERED

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3 <110> APPLICANT: LIVSHITS, VITALIY
4   ZAKATAEVA, NATALIA
5   NAKANISHI, KAZUO
6   VENIAMINOVICH, VLADIMIR
7   TROSHIN, PETR
8   TOKHMAKOVA, IRINA
10 <120> TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACIDS
12 <130> FILE REFERENCE: 0010-1066-0
14 <140> CURRENT APPLICATION NUMBER: 09/459,573
15 <141> CURRENT FILING DATE: 1999-12-13
17 <150> PRIOR APPLICATION NUMBER: RU98124016
18 <151> PRIOR FILING DATE: 1998-12-30
20 <150> PRIOR APPLICATION NUMBER: RU99104431
21 <151> PRIOR FILING DATE: 1999-03-09
23 <160> NUMBER OF SEQ ID NOS: 24
25 <170> SOFTWARE: PatentIn version 3.0
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29 <212> TYPE: DNA
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33 <221> NAME/KEY: misc_feature
34 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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70 <211> LENGTH: 27
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence

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76 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA  

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145 <221> NAME/KEY: CDS  

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148 <400> SEQUENCE: 9

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150 Met Met Gln Leu Val His Leu Phe Met Asp Glu Ile Thr Met Asp Pro	
151 1 5 10 15	
153 ttg cat gcc gtt tac ctg acc gta gga ctg ttc gtg att act ttt ttt	96
154 Leu His Ala Val Tyr Leu Thr Val Gly Leu Phe Val Ile Thr Phe Phe	
155 20 25 30	
157 aat ccg gga gcc aat ctc ttt gtg gta gta caa acc agc ctg gct tcc	144
158 Asn Pro Gly Ala Asn Leu Phe Val Val Val Gln Thr Ser Leu Ala Ser	
159 35 40 45	
161 ggt cga cgc gca ggg gtg ctg acc ggg ctg ggc gtg gcg ctg ggc gat	192
162 Gly Arg Arg Ala Gly Val Leu Thr Gly Leu Gly Val Ala Leu Gly Asp	
163 50 55 60	
165 gca ttt tat tcc ggg ttg ggt ttg ttt ggt ctt gca acg cta att acg	240
166 Ala Phe Tyr Ser Gly Leu Gly Leu Phe Gly Leu Ala Thr Leu Ile Thr	
167 65 70 75 80	
169 cag tgt gag gag att ttt tcg ctt atc aga atc gtc ggc ggc gct tat	288
170 Gln Cys Glu Glu Ile Phe Ser Leu Ile Arg Ile Val Gly Gly Ala Tyr	
171 85 90 95	
173 ctc tta tgg ttt gcg tgg tgc agc atg cgc cgc cag tca aca ccg caa	336
174 Leu Leu Trp Phe Ala Trp Cys Ser Met Arg Arg Gln Ser Thr Pro Gln	
175 100 105 110	
177 atg agc aca cta caa caa ccg att agc gcc ccc tgg tat gtc ttt ttt	384
178 Met Ser Thr Leu Gln Gln Pro Ile Ser Ala Pro Trp Tyr Val Phe Phe	
179 115 120 125	
181 cgc cgc gga tta att acc gat ctc tct aac ccg caa acc gtt tta ttt	432
182 Arg Arg Gly Leu Ile Thr Asp Leu Ser Asn Pro Gln Thr Val Leu Phe	
183 130 135 140	
185 ttt atc agt att ttc tca gta aca tta aat gcc gaa aca cca aca tgg	480
186 Phe Ile Ser Ile Phe Ser Val Thr Leu Asn Ala Glu Thr Pro Thr Trp	
187 145 150 155 160	
189 gca cgt tta atg gcc tgg gcg ggg att gtg ctc gca tca att atc tgg	528
190 Ala Arg Leu Met Ala Trp Ala Gly Ile Val Leu Ala Ser Ile Ile Trp	
191 165 170 175	
193 cga gtt ttt ctt agt cag gcg ttt tct ttg ccc gct gtg cgt cgt gct	576
194 Arg Val Phe Leu Ser Gln Ala Phe Ser Leu Pro Ala Val Arg Arg Ala	
195 180 185 190	
197 tat ggg cgt atg caa cgc gtt gcc agt cgg gtt att ggt gca att att	624
198 Tyr Gly Arg Met Gln Arg Val Ala Ser Arg Val Ile Gly Ala Ile Ile	
199 195 200 205	
201 ggt gta ttc gcg cta cgc ctg att tac gaa ggg gtg acg cag cgg tga	672
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217	Leu	His	Ala	Val	Tyr	Leu	Thr	Val	Gly	Leu	Phe	Val	Ile	Thr	Phe	Phe
218	20					25							30			
221	Asn	Pro	Gly	Ala	Asn	Leu	Phe	Val	Val	Val	Gln	Thr	Ser	Leu	Ala	Ser
222	35					40						45				
225	Gly	Arg	Arg	Ala	Gly	Val	Leu	Thr	Gly	Leu	Gly	Val	Ala	Leu	Gly	Asp
226	50					55					60					
229	Ala	Phe	Tyr	Ser	Gly	Leu	Gly	Leu	Phe	Gly	Leu	Ala	Thr	Leu	Ile	Thr
230	65					70				75			80			
233	Gln	Cys	Glu	Glu	Ile	Phe	Ser	Leu	Ile	Arg	Ile	Val	Gly	Gly	Ala	Tyr
234		85							90				95			
237	Leu	Leu	Trp	Phe	Ala	Trp	Cys	Ser	Met	Arg	Arg	Gln	Ser	Thr	Pro	Gln
238		100						105					110			
241	Met	Ser	Thr	Leu	Gln	Gln	Pro	Ile	Ser	Ala	Pro	Trp	Tyr	Val	Phe	Phe
242		115						120					125			
245	Arg	Arg	Gly	Leu	Ile	Thr	Asp	Leu	Ser	Asn	Pro	Gln	Thr	Val	Leu	Phe
246		130					135					140				
249	Phe	Ile	Ser	Ile	Phe	Ser	Val	Thr	Leu	Asn	Ala	Glu	Thr	Pro	Thr	Trp
250	145					150				155			160			
253	Ala	Arg	Leu	Met	Ala	Trp	Ala	Gly	Ile	Val	Leu	Ala	Ser	Ile	Ile	Trp
254		165						170			175					
257	Arg	Val	Phe	Leu	Ser	Gln	Ala	Phe	Ser	Leu	Pro	Ala	Val	Arg	Arg	Ala
258		180						185					190			
261	Tyr	Gly	Arg	Met	Gln	Arg	Val	Ala	Ser	Arg	Val	Ile	Gly	Ala	Ile	Ile
262		195						200					205			
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281	1			5				10				15				
283	gcc	att	ttt	att	gtg	ttg	gtg	cca	ggg	cca	aat	acc	ctg	ttt	gta	ctc
284	Ala	Ile	Phe	Ile	Val	Leu	Val	Pro	Gly	Pro	Asn	Thr	Leu	Phe	Val	Leu
285		20				25						30				
287	aaa	aat	agc	gtc	agt	agc	ggt	atg	aaa	ggc	ggt	tat	ctt	gcg	gcc	tgc
288	Lys	Asn	Ser	Val	Ser	Ser	Gly	Met	Lys	Gly	Gly	Tyr	Leu	Ala	Ala	Cys
289		35				40					45					
291	ggt	gta	ttt	att	ggc	gat	gcf	gta	ttg	atg	ttt	ctg	gca	tgg	gct	gga
292	Gly	Val	Phe	Ile	Gly	Asp	Ala	Val	Leu	Met	Phe	Leu	Ala	Trp	Ala	Gly
293		50				55				60						
295	gtg	gcf	aca	tta	att	aag	acc	acc	ccg	ata	tta	ttc	aac	att	gta	cgt
296	Val	Ala	Thr	Leu	Ile	Lys	Thr	Thr	Pro	Ile	Leu	Phe	Asn	Ile	Val	Arg
297	65					70				75			80			

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299 tat ctt ggt gcg ttt tat ttg ctc tat ctg ggg agt aaa att ctt tac	288
300 Tyr Leu Gly Ala Phe Tyr Leu Leu Tyr Leu Gly Ser Lys Ile Leu Tyr	
301 85 90 95	
303 gcg acc ctg aag ggt aaa aat agc gag gcc aaa tcc gat gag ccc caa	336
304 Ala Thr Leu Lys Gly Lys Asn Ser Glu Ala Lys Ser Asp Glu Pro Gln	
305 100 105 110	
307 tac ggt gct att ttt aaa cgc gcg tta att ttg agc ctg act aat ccg	384
308 Tyr Gly Ala Ile Phe Lys Arg Ala Leu Ile Leu Ser Leu Thr Asn Pro	
309 115 120 125	
311 aaa gcc att ttg ttc tat gtg tcg ttt ttc gta cag ttt atc gat gtt	432
312 Lys Ala Ile Leu Phe Tyr Val Ser Phe Val Gln Phe Ile Asp Val	
313 130 135 140	
315 aat gcc cca cat acg gga att tca ttc ttt att ctg gcg gcg acg ctg	480
316 Asn Ala Pro His Thr Gly Ile Ser Phe Phe Ile Leu Ala Ala Thr Leu	
317 145 150 155 160	
319 gaa ctg gtg agt ttc tgc tat ttg agc ttc ctg att ata tct ggt gct	528
320 Glu Leu Val Ser Phe Cys Tyr Leu Ser Phe Leu Ile Ile Ser Gly Ala	
321 165 170 175	
323 ttt gtc acg cag tac ata cgt acc aaa aag aaa ctg gct aaa gtt ggc	576
324 Phe Val Thr Gln Tyr Ile Arg Thr Lys Lys Leu Ala Lys Val Gly	
325 180 185 190	
327 aac tca ctg att ggt ttg atg ttc gtg ggt ttc gct gcc cga ctg gcg	624
328 Asn Ser Leu Ile Gly Leu Met Phe Val Gly Phe Ala Ala Arg Leu Ala	
329 195 200 205	
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332 Thr Leu Gln Ser	
333 210	
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339 <213> ORGANISM: Escherichia coli	
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348 20 25 30	
351 Lys Asn Ser Val Ser Ser Gly Met Lys Gly Gly Tyr Leu Ala Ala Cys	
352 35 40 45	
355 Gly Val Phe Ile Gly Asp Ala Val Leu Met Phe Leu Ala Trp Ala Gly	
356 50 55 60	
359 Val Ala Thr Leu Ile Lys Thr Thr Pro Ile Leu Phe Asn Ile Val Arg	
360 65 70 75 80	
363 Tyr Leu Gly Ala Phe Tyr Leu Leu Tyr Leu Gly Ser Lys Ile Leu Tyr	
364 85 90 95	
367 Ala Thr Leu Lys Gly Lys Asn Ser Glu Ala Lys Ser Asp Glu Pro Gln	
368 100 105 110	
371 Tyr Gly Ala Ile Phe Lys Arg Ala Leu Ile Leu Ser Leu Thr Asn Pro	
372 115 120 125	
375 Lys Ala Ile Leu Phe Tyr Val Ser Phe Phe Val Gln Phe Ile Asp Val	

VERIFICATION SUMMARY
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